



1600

## RAW SEQUENCE LISTING

DATE: 02/08/2002

PATENT APPLICATION: US/09/308,435B

TIME: 10:35:22

Input Set : N:\Crf3\Refhold\I308435B.raw

Output Set: N:\CRF3\02082002\I308435B.raw

C--> 1 <110> APPLICANT: Astra Aktiebolag  
C--> 2 <120> TITLE OF INVENTION: Vaccine Delivery System and Method of Production  
3 <130> FILE REFERENCE: 1103326-0560  
4 <140> CURRENT APPLICATION NUMBER: US/09/308,435B  
5 <141> CURRENT FILING DATE: 1999-04-09  
6 <150> PRIOR APPLICATION NUMBER: PCT/SE99/00582  
7 <151> PRIOR FILING DATE: 1999-04-09  
8 <150> PRIOR APPLICATION NUMBER: SE 9801288-3  
9 <151> PRIOR FILING DATE: 1998-04-14  
10 <160> NUMBER OF SEQ ID NOS: 25  
11 <170> SOFTWARE: PatentIn Ver. 2.1  
13 <210> SEQ ID NO: 1  
14 <211> LENGTH: 1670  
15 <212> TYPE: DNA  
16 <213> ORGANISM: Helicobacter pylori  
17 <220> FEATURE:  
18 <221> NAME/KEY: CDS  
19 <222> LOCATION: (793)..(1572)  
20 <400> SEQUENCE: 1

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23 gatttgattt tagggaatta catgcaagtg aatgaaaaaa acattcaagc gtttgccccc 180  
24 aaacaataag gtaaaaaatg ccaactcactc atttgaatga agaaaaatcaa cctaaaaatgg 240  
25 tggatatagg ggataaagaa accactgaaa gaatcgctct agcaagcggg cgtatcagca 300  
26 tgaataaaga ggcttatgac gctattatca atcatggcgt caaaaagggg ccggtattac 360  
27 aaactgctat tattgctggg attatggggg ctaaaaagac aagcgaactc attcccatgt 420  
28 gccatccaat catgctcaat ggggtggata ttgatatttt agaagaaaaa gagacttgta 480  
29 gttttaaact ctatgcgaga gtcaaaactc aagctaaaac gggcgtagaa atggaagcgc 540  
30 taatgagtgt gagcgtaggg cttttaacca tttatgacat ggtgaaagcc attgataaga 600  
31 gcatgacaat tagcgggtgtg atgctggaat ataaaagtgg aggcaaaagt ggggattata 660  
32 acgctaaaaa atagaaaaag actgataatc taaagatatt agggtaaaat aacattttga 720  
33 caacaaaagc gtgttggttg cttcggattt gttgttatag aagtctaaaa tattacaatc 780  
34 aaggatagaa cg atg aga gca aat aat cat ttt aaa gat ttt gca tgg aaa 831  
35 Met Arg Ala Asn Asn His Phe Lys Asp Phe Ala Trp Lys  
36 1 5 10  
37 aaa tgc ctt tta ggc gcg agc gtg gtg gct tta tta gtg gga tgc agc 879  
38 Lys Cys Leu Leu Gly Ala Ser Val Val Ala Leu Leu Val Gly Cys Ser  
39 15 20 25  
40 ccg cat att att gaa acc aat gaa gtc gct ttg aaa ttg aat tac cat 927  
41 Pro His Ile Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His  
42 30 35 40 45  
43 cca gct agc gag aaa gtt caa gcg tta gat gaa aag att ttg ctt tta 975  
44 Pro Ala Ser Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu Leu

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46  agg oca gct ttc caa tat agc gat aat atc gct aaa gag tat gaa aac 1023
47  Arg Pro Ala Phe Gln Tyr Ser Asp Asn Ile Ala Lys Glu Tyr Glu Asn
48          65          70          75
49  aaa ttc aag aat caa acc gcg ctc aag gtt gaa cag att ttg caa aat 1071
50  Lys Phe Lys Asn Gln Thr Ala Leu Lys Val Glu Gln Ile Leu Gln Asn
51          80          85          90
52  caa ggc tat aag gtt att agc gta gat agc agc gat aaa gac gat ttt 1119
53  Gln Gly Tyr Lys Val Ile Ser Val Asp Ser Ser Asp Lys Asp Asp Phe
54          95          100          105
55  tct ttt gca caa aaa aaa gaa ggg tat ttg gcg gtt gct atg aat ggc 1167
56  Ser Phe Ala Gln Lys Lys Glu Gly Tyr Leu Ala Val Ala Met Asn Gly
57  110          115          120          125
58  gaa att gtt tta cgc ccc gat cct aaa agg acc ata cag aaa aaa tca 1215
59  Glu Ile Val Leu Arg Pro Asp Pro Lys Arg Thr Ile Gln Lys Lys Ser
60          130          135          140
61  gaa ccc ggg tta tta ttc tcc acc ggt ttg gac aaa atg gaa ggg gtt 1263
62  Glu Pro Gly Leu Leu Phe Ser Thr Gly Leu Asp Lys Met Glu Gly Val
63          145          150          155
64  tta atc ccg gct ggg ttt att aag gtt acc ata cta gag cct atg agt 1311
65  Leu Ile Pro Ala Gly Phe Ile Lys Val Thr Ile Leu Glu Pro Met Ser
66          160          165          170
67  ggg gaa tct ttg gat tct ttt acg atg gat ttg agc gag ttg gac att 1359
68  Gly Glu Ser Leu Asp Ser Phe Thr Met Asp Leu Ser Glu Leu Asp Ile
69          175          180          185
70  caa gaa aaa ttc tta aaa acc acc cat tca agc cat agc ggg ggg tta 1407
71  Gln Glu Lys Phe Leu Lys Thr Thr His Ser Ser His Ser Gly Gly Leu
72  190          195          200          205
73  gtt agc act atg gtt aag gga acg gat aat tct aat gac gcg atc aag 1455
74  Val Ser Thr Met Val Lys Gly Thr Asp Asn Ser Asn Asp Ala Ile Lys
75          210          215          220
76  agc gct ttg aat aag att ttt gca aat atc atg caa gaa ata gac aaa 1503
77  Ser Ala Leu Asn Lys Ile Phe Ala Asn Ile Met Gln Glu Ile Asp Lys
78          225          230          235
79  aaa ctc act caa aag aat tta gaa tct tat caa aaa gac gcc aaa gaa 1551
80  Lys Leu Thr Gln Lys Asn Leu Glu Ser Tyr Gln Lys Asp Ala Lys Glu
81          240          245          250
82  tta aaa ggc aaa aga aac cga taaaaacaaa taacgcataa gaaaagaacg 1602
83  Leu Lys Gly Lys Arg Asn Arg
84          255          260
85  ctggaataaaa ctgcttaaaa aggggttttt agcgtttcttt ttgagcgtgt atttaagggc 1662
86  tgatgatc 1670
88 <210> SEQ ID NO: 2
89 <211> LENGTH: 260
90 <212> TYPE: PRT
91 <213> ORGANISM: Helicobacter pylori
92 <400> SEQUENCE: 2
93  Met Arg Ala Asn Asn His Phe Lys Asp Phe Ala Trp Lys Lys Cys Leu
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95   Leu Gly Ala Ser Val Val Ala Leu Leu Val Gly Cys Ser Pro His Ile
96               20               25               30
97   Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His Pro Ala Ser
98               35               40               45
99   Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu Leu Arg Pro Ala
100          50          55          60
101   Phe Gln Tyr Ser Asp Asn Ile Ala Lys Glu Tyr Glu Asn Lys Phe Lys
102          65          70          75          80
103   Asn Gln Thr Ala Leu Lys Val Glu Gln Ile Leu Gln Asn Gln Gly Tyr
104          85          90          95
105   Lys Val Ile Ser Val Asp Ser Ser Asp Lys Asp Asp Phe Ser Phe Ala
106          100         105         110
107   Gln Lys Lys Glu Gly Tyr Leu Ala Val Ala Met Asn Gly Glu Ile Val
108          115         120         125
109   Leu Arg Pro Asp Pro Lys Arg Thr Ile Gln Lys Lys Ser Glu Pro Gly
110          130         135         140
111   Leu Leu Phe Ser Thr Gly Leu Asp Lys Met Glu Gly Val Leu Ile Pro
112          145         150         155         160
113   Ala Gly Phe Ile Lys Val Thr Ile Leu Glu Pro Met Ser Gly Glu Ser
114          165         170         175
115   Leu Asp Ser Phe Thr Met Asp Leu Ser Glu Leu Asp Ile Gln Glu Lys
116          180         185         190
117   Phe Leu Lys Thr Thr His Ser Ser His Ser Gly Gly Leu Val Ser Thr
118          195         200         205
119   Met Val Lys Gly Thr Asp Asn Ser Asn Asp Ala Ile Lys Ser Ala Leu
120          210         215         220
121   Asn Lys Ile Phe Ala Asn Ile Met Gln Glu Ile Asp Lys Lys Leu Thr
122          225         230         235         240
123   Gln Lys Asn Leu Glu Ser Tyr Gln Lys Asp Ala Lys Glu Leu Lys Gly
124          245         250         255
125   Lys Arg Asn Arg
126          260

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128 &lt;210&gt; SEQ ID NO: 3

129 &lt;211&gt; LENGTH: 1670

130 &lt;212&gt; TYPE: DNA

131 &lt;213&gt; ORGANISM: Helicobacter pylori

132 &lt;220&gt; FEATURE:

133 &lt;221&gt; NAME/KEY: CDS

134 &lt;222&gt; LOCATION: (793)..(1572)

135 &lt;400&gt; SEQUENCE: 3

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136   gatactatcg cgccaaaggt ggtattagga ataagagctt gattattaat ctccctggta 60
137   agtccaaaaa gtattagaga atgcttagag gcggtttttc cagcgattcc ttattgcgtg 120
138   gatttgattt tagggaatta catgcaagtg aatgaaaaaa acattcaagc gtttgccccc 180
139   aaacaataag gtaaaaaatg ccaactcactc atttgaatga agaaaatcaa ctaaaaatgg 240
140   tggatatagg ggataaagaa accactgaaa gaatcgctct agcaagcggg cgtatcagca 300
141   tgaataaaga ggcttatgac gctattatca atcatggcgt caaaaagggt ccggtattac 360
142   aaactgctat tattgctggg attatggggg ctaaaaagac aagcgaactc attcccatgt 420
143   gccatccaat catgctcaat ggggtggata ttgatatttt agaagaaaaa gagacttgta 480
144   gttttaaact ctatgcgaga gtcaaaaactc aagctaaaac gggcgtagaa atggaagcgc 540

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146 gcatgacaat tagcgggtgtg atgctggaat ataaaagtgg aggcaaaagt ggggattata 660
147 acgctaaaaa atagaaaaaag actgataatc taaagatatt agggtaaaat aacattttga 720
148 caacaaaagc gtgttggttg cttcggattt gttgttatag aagtctaaaa tattacaatc 780
149 aaggatagaa cg atg aga gca aat aat cat ttt aaa gat ttt gca tgg aaa 831
150 Met Arg Ala Asn Asn His Phe Lys Asp Phe Ala Trp Lys
151      1      5      10
152 aaa tgc ctt tta ggc gcg agc gtg gtg gct tta tta gtg gga tgc agc 879
153 Lys Cys Leu Leu Gly Ala Ser Val Val Ala Leu Leu Val Gly Cys Ser
154      15      20      25
155 ccg cat att att gaa acc aat gaa gtc gct ttg aaa ttg aat tac cat 927
156 Pro His Ile Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His
157      30      35      40      45
158 cca gct agc gag aaa gtt caa gcg tta gat gaa aag att ttg ctt tta 975
159 Pro Ala Ser Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu Leu
160      50      55      60
161 agg cca gct ttc caa tat agc gat aat atc gct aaa gag tat gaa aac 1023
162 Arg Pro Ala Phe Gln Tyr Ser Asp Asn Ile Ala Lys Glu Tyr Glu Asn
163      65      70      75
164 aaa ttc aag aat caa acc gcg ctc aag gtt gaa cag att ttg caa aat 1071
165 Lys Phe Lys Asn Gln Thr Ala Leu Lys Val Glu Gln Ile Leu Gln Asn
166      80      85      90
167 caa ggc tat aag gtt att agc gta gat agc agc gat aaa gac gat ttt 1119
168 Gln Gly Tyr Lys Val Ile Ser Val Asp Ser Ser Asp Lys Asp Asp Phe
169      95      100      105
170 tct ttt gca caa aaa aaa gaa ggg tat ttg gcg gtt gct atg aat ggc 1167
171 Ser Phe Ala Gln Lys Lys Glu Gly Tyr Leu Ala Val Ala Met Asn Gly
172      110      115      120      125
173 gaa att gtt tta cgc ccc gat cct aaa agg acc ata cag aaa aaa tca 1215
174 Glu Ile Val Leu Arg Pro Asp Pro Lys Arg Thr Ile Gln Lys Lys Ser
175      130      135      140
176 gaa ccc ggg tta tta ttc tcc acc ggt ttg gac aaa atg gaa ggg gtt 1263
177 Glu Pro Gly Leu Leu Phe Ser Thr Gly Leu Asp Lys Met Glu Gly Val
178      145      150      155
179 tta atc ccg gct ggg ttt att aag gtt acc ata cta gag cct atg agt 1311
180 Leu Ile Pro Ala Gly Phe Ile Lys Val Thr Ile Leu Glu Pro Met Ser
181      160      165      170
182 ggg gaa tct ttg gat tct ttt acg atg gat ttg agc gag ttg gac att 1359
183 Gly Glu Ser Leu Asp Ser Phe Thr Met Asp Leu Ser Glu Leu Asp Ile
184      175      180      185
185 caa gaa aaa ttc tta aaa acc acc cat tca agc cat agc ggg ggg tta 1407
186 Gln Glu Lys Phe Leu Lys Thr Thr His Ser Ser His Ser Gly Gly Leu
187      190      195      200      205
188 gtt agc act atg gtt aag gga acg gat aat tct aat gac gcg atc aag 1455
189 Val Ser Thr Met Val Lys Gly Thr Asp Asn Ser Asn Asp Ala Ile Lys
190      210      215      220
191 aga gct ttg aat aag att ttt gca aat atc atg caa gaa ata gac aaa 1503
192 Arg Ala Leu Asn Lys Ile Phe Ala Asn Ile Met Gln Glu Ile Asp Lys
193      225      230      235

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194   aaa ctc act caa aag aat tta gaa tct tat caa aaa gac gcc aaa gaa   1551
195   Lys Leu Thr Gln Lys Asn Leu Glu Ser Tyr Gln Lys Asp Ala Lys Glu
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198   Leu Lys Gly Lys Arg Asn Arg
199           255                      260
200   cttgaataaaa ctgcttaaaaa aggggtttttt agcggttcttt ttgagcgtgt atttaagggc 1662
201   tgatgatc   1670
203 <210> SEQ ID NO: 4
204 <211> LENGTH: 260
205 <212> TYPE: PRT
206 <213> ORGANISM: Helicobacter pylori
207 <400> SEQUENCE: 4
208   Met Arg Ala Asn Asn His Phe Lys Asp Phe Ala Trp Lys Lys Cys Leu
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211           20             25             30
212   Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His Pro Ala Ser
213           35             40             45
214   Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu Leu Arg Pro Ala
215           50             55             60
216   Phe Gln Tyr Ser Asp Asn Ile Ala Lys Glu Tyr Glu Asn Lys Phe Lys
217           65             70             75             80
218   Asn Gln Thr Ala Leu Lys Val Glu Gln Ile Leu Gln Asn Gln Gly Tyr
219           85             90             95
220   Lys Val Ile Ser Val Asp Ser Ser Asp Lys Asp Asp Phe Ser Phe Ala
221           100            105            110
222   Gln Lys Lys Glu Gly Tyr Leu Ala Val Ala Met Asn Gly Glu Ile Val
223           115            120            125
224   Leu Arg Pro Asp Pro Lys Arg Thr Ile Gln Lys Lys Ser Glu Pro Gly
225           130            135            140
226   Leu Leu Phe Ser Thr Gly Leu Asp Lys Met Glu Gly Val Leu Ile Pro
227           145            150            155            160
228   Ala Gly Phe Ile Lys Val Thr Ile Leu Glu Pro Met Ser Gly Glu Ser
229           165            170            175
230   Leu Asp Ser Phe Thr Met Asp Leu Ser Glu Leu Asp Ile Gln Glu Lys
231           180            185            190
232   Phe Leu Lys Thr Thr His Ser Ser His Ser Gly Gly Leu Val Ser Thr
233           195            200            205
234   Met Val Lys Gly Thr Asp Asn Ser Asn Asp Ala Ile Lys Arg Ala Leu
235           210            215            220
236   Asn Lys Ile Phe Ala Asn Ile Met Gln Glu Ile Asp Lys Lys Leu Thr
237           225            230            235            240
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240   Lys Arg Asn Arg
241           260
243 <210> SEQ ID NO: 5
244 <211> LENGTH: 60

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VERIFICATION SUMMARY

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Output Set: N:\CRF3\02082002\I308435B.raw

L:4 M:270 C: Current Application Number differs, Wrong Format

L:5 M:271 C: Current Filing Date differs, Replaced Current Filing Date